

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Fri May 11 11:30:14 EDT 2007

=====

Application No: 10564446

Version No: 1.1

Input Set:

Output Set:

Started: 2007-05-11 11:29:55.559
Finished: 2007-05-11 11:29:55.961
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 402 ms
Total Warnings: 24
Total Errors: 0
No. of SeqIDs Defined: 32
Actual SeqID Count: 32

ErrCode	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION MANAGER OF NATIONAL INSTITUTE OF INFECTIOUS DISEASES

Hanada, Kentaro
Nishijima, Masahiro
Kumagai, Keigo

<120> DRUG PROMOTING CERAMIDE TRANSPORT, BASE SEQUENCE FOR PRODUCING THE DRUG, METHOD OF MEASURING ACTIVITY OF PROMOTING CERAMIDE RELEASE AND METHOD OF MEASURING ACTIVITY OF PROMOTING INTERMEMBRANE CERAMIDE TRANSFER

<130> 283729US0X PCT

<140> 10/564,446

<141> 2006-01-12

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 598

<212> PRT

<213> HeLa cell

<400> 1

Met	Ser	Asp	Asn	Gln	Ser	Trp	Asn	Ser	Ser	Gly	Ser	Glu	Glu	Asp	Pro
1				5					10					15	

Glu	Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg	Cys	Gly	Val	Leu	Ser	Lys
			20					25					30		

Trp	Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp	Arg	Trp	Val	Val	Leu	Lys
		35					40					45			

Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly
	50					55					60				

Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	Val	Ile	Thr	Pro	His	Asp
65					70					75				80	

Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	Asn	Asp	Ser	Val	Trp	Tyr
				85					90					95	

Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	Gln	Trp	Ile	Asp	Ala	Ile
			100					105					110		

Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	Ser	Glu	Ser	Ser	Leu	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115

120

125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
 130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
 145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
 165 170 175

Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
 180 185 190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
 195 200 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
 210 215 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
 225 230 235 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
 245 250 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
 260 265 270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
 275 280 285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
 290 295 300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
 305 310 315 320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
 325 330 335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
 340 345 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
355 360 365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
370 375 380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
385 390 395 400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
405 410 415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
420 425 430

Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
435 440 445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
450 455 460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465 470 475 480

Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
485 490 495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
500 505 510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
515 520 525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
530 535 540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545 550 555 560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
565 570 575

Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
580 585 590

Gly Lys Pro Ile Leu Phe
595

<210> 2
<211> 624
<212> PRT
<213> HeLa cell

<400> 2

Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
1 5 10 15

Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
20 25 30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65 70 75 80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
85 90 95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115 120 125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp

165	170	175
Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp		
180	185	190
Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro		
195	200	205
Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys		
210	215	220
Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp		
225	230	235 240
Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu		
245	250	255
Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser		
260	265	270
Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu		
275	280	285
Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe		
290	295	300
Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu		
305	310	315 320
Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile		
325	330	335
Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser		
340	345	350
Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val		
355	360	365
Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val		
370	375	380
Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met		
385	390	395 400

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
405 410 415

Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
420 425 430

Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
435 440 445

Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
450 455 460

Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465 470 475 480

Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
485 490 495

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
500 505 510

Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
515 520 525

Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
530 535 540

Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545 550 555 560

Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
565 570 575

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
580 585 590

Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
595 600 605

Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
610 615 620

<210> 3
<211> 598
<212> PRT
<213> CHO-K1

<400> 3

Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
1 5 10 15

Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
20 25 30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

Asn Asn Thr Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65 70 75 80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
85 90 95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115 120 125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165 170 175

Thr Leu Gln Lys Tyr Phe Asp Val Cys Ala Asp Ala Val Ser Lys Asp
180 185 190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro

195

200

205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Asn Thr Asn Gly Asn Lys
 210 215 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
 225 230 235 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
 245 250 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Glu Ser
 260 265 270

Trp Gln Lys Arg His Asp Lys Glu Met Glu Lys Arg Arg Arg Leu Glu
 275 280 285

Glu Ala Tyr Lys Asn Ala Met Ala Glu Leu Lys Lys Lys Pro Arg Phe
 290 295 300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
 305 310 315 320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
 325 330 335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Pro
 340 345 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
 355 360 365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
 370 375 380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
 385 390 395 400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
 405 410 415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
 420 425 430

Cys Asn Tyr Phe Trp Ser Val Asp Val Arg Asn Asp Trp Glu Thr Thr
435 440 445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
450 455 460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465 470 475 480

Leu Tyr Leu Ser Ala Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
485 490 495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
500 505 510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
515 520 525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
530 535 540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545 550 555 560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
565 570 575

Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
580 585 590

Gly Lys Pro Ile Leu Phe
595

<210> 4

<211> 624

<212> PRT

<213> CHO-K1

<400> 4

Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
1 5 10 15

Glu	Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg	Cys	Gly	Val	Leu	Ser	Lys	20	25	30	
Trp	Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp	Arg	Trp	Val	Val	Leu	Lys	35	40	45	
Asn	Asn	Thr	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly	50	55	60	
Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	Val	Ile	Thr	Pro	His	Asp	65	70	75	80
Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	Asn	Asp	Ser	Val	Trp	Tyr	85	90	95	
Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	Gln	Trp	Ile	Asp	Ala	Ile	100	105	110	
Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	Ser	Glu	Ser	Ser	Leu	Arg	115	120	125	
Arg	His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser	Gly	Ala	Ser	Gly	Tyr	Ser	130	135	140	
Ala	Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly	His	Ser	Leu	Arg	Glu	Lys	145	150	155	160
Leu	Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile	Leu	Cys	Arg	Gln	Val	Asp	165	170	175	
Thr	Leu	Gln	Lys	Tyr	Phe	Asp	Val	Cys	Ala	Asp	Ala	Val	Ser	Lys	Asp	180	185	190	
Glu	Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	As										